

ERIN E. MURPHY, JANE D. MATTSON,
ELIZABETH ESTHER MARY BATES,
DANIEL M. GORMAN and SERGE J.E.

PATENT

LEBECQUE
Application No.:
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Please also amend the specification by deleting Sequence Submission pp. 84-110, and substitute therefore the attached Sequence Submission, pp. 84-108.

REMARKS

The amendments to the related application section provide the filing dates for the individual priority applications from which this application claims benefit.

The amendments to the sequence listing correct various formalities in the originally filed listing of the parent application. No new matter is added thereby.

The Applicants also attach a request under 37 C.F.R. § 1.821(e) that the computer-readable form filed in the parent Application No. 09/351,777 be used as the computer-readable form for the instant application.

I hereby state that the informational contents of the paper and computer readable copies of the above Sequence Listing are believed to be the same. This submission involves no new matter as the enclosed sequences are the same as those filed in the priority documents.

CONCLUSION

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,


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VERSION WITH MARKINGS TO SHOW CHANGES

In the Specification:

This application is a Continuation Application of U.S. Patent Utility Application No. 09/351,777 filed on July 12, 1999. USSN 09/351,777 was a conversion to a U.S. Utility Patent Application of U.S. Provisional Patent Application of USSN 60/092,658 which was filed on July 13, 1998; USSN 60/093,897 which was filed on July 23, 1998; and USSN 60/099,999 which was filed on September 11, 1998. This application incorporates herein by reference, and claims priority to, each of these four applications. [This filing is a conversion to a U.S. Utility Patent Application of U.S. Provisional Patent Applications USSN 60/092,658; USSN 60/093,897; and USSN 60/099,999; each of which is incorporated herein by reference].

SEQUENCE SUBMISSION

Sub A2

SEQ ID NO: 1 is a primate HDTEA84 nucleic acid sequence.
SEQ ID NO: 2 is a primate HDTEA84 amino acid sequence.
5 SEQ ID NO: 3 is a primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 4 is a primate HSLJD37R amino acid sequence.
SEQ ID NO: 5 is supplemented primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 6 is supplemented primate HSLJD37R amino acid sequence.
10 SEQ ID NO: 7 is variant primate HSLJD37R nucleic acid sequence.
SEQ ID NO: 8 is variant primate HSLJD37R amino acid sequence.
SEQ ID NO: 9 is murine TNF-R2 amino acid sequence.
SEQ ID NO: 10 is human TNF-R2 amino acid sequence.
SEQ ID NO: 11 is human ORG amino acid sequence.
15 SEQ ID NO: 12 is a rodent RANKL nucleic acid sequence.
SEQ ID NO: 13 is a rodent RANKL amino acid sequence.
SEQ ID NO: 14 is a primate RANKL nucleic acid sequence.
SEQ ID NO: 15 is a primate RANKL amino acid sequence.
20 SEQ ID NO: 16 is another primate RANKL nucleic acid sequence.
SEQ ID NO: 17 is another primate RANKL amino acid sequence.
SEQ ID NO: 18 is a variant primate RANKL nucleic acid sequence.
SEQ ID NO: 19 is a variant primate RANKL amino acid sequence.

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Mattson, Jeanine D.
Bates, Elizabeth Esther Mary
Gorman, Daniel M.
Lebecque, Serge J.E.

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Sulf A2

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Sub A2

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Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
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depends on genetic code

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Sulf A2

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tgttgtgaaa	tacccaccac	taaagttttt	taagttccat	attttctcca	ttttgccttc											2684	
25	ttatgtatTTT	tcaagattat	tctgtgcact	ttaaatttac	tcaacttacc	ataaatgcag											2744
tgtgactttt	cccacacact	ggattgtgag	gctcttaact	tcttaaaaagt	ataatggcat											2804	
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Ile	Ala	Arg	Arg	Ala	Thr	Ala	Thr	Met	Ile	Ala	Gly	Ser	Leu	Leu	Leu		
-25								-20			-15				-10		
45	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	Lys	Ala	Ser	
								-5		-1	1			5			
50	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	Thr	Gly	Gln	Val	
								10		15				20			
55	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	Val	Ser	Glu	His	Cys	
								25		30			35				
60	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	Cys	Pro	Val	Gly	Thr	Phe	
								40		45			50			55	
	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	Cys	His	Asp	Cys	Ser	Gln	Pro	
								60		65			70				
65	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	

Sub A2

	75	80	85
	Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys		
	90 95 100		
5	Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly		
	105 110 115		
10	Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe		
	120 125 130 135		
	Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys		
	140 145 150		
15	Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp		
	155 160 165		
	Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser		
	170 175 180		
20	Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu		
	185 190 195		
25	Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser		
	200 205 210 215		
	Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu		
	220 225 230		
30	Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val		
	235 240 245		
	Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro		
	250 255 260		
35	His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly		
	265 270 275		
40	Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro		
	280 285 290 295		
	Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp		
	300 305 310		
45	Met Ile Val Leu Phe Leu Leu Val Leu Val Val Ile Val Val Cys		
	315 320 325		
	Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp		
	330 335 340		
50	Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro		
	345 350 355		
	Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile		
	360 365 370 375		
	Asp Ile Leu Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp		
	380 385 390		
60	Ile Tyr Gln Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe		

395 400 405

Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln
410 415 420

5 His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser
425 430 435

Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg Gly
10 440 445 450 455

Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro
460 465 470

15 Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro Asn Ala
475 480 485

Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro Gln Asp
490 495 500

20 Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu Arg Cys
505 510 515

Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe
25 520 525 530 535

Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp
540 545 550

30 Pro Cys Asp Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe Leu Asn
555 560 565

Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys
570 575 580

35 Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser
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Gln Thr Leu Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu
40 600 605 610

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Met Gly Thr Ser Pro Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

Sub A2

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atc gct cgc cga gcc aca gcc acg atg atc gct ggc tcc ctt ctc ctg 96
Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25 -20 -15 -10
ctt gga ttc ctt agc acc acc aca gct cag cca gaa cag aag gcc tcg 144
Leu Gly Phe Leu Ser Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
-5 -1 1 5
aat ctc att ggc aca tac cgc cat gtt gac cgt gcc acc ggc cag gtg 192
Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20
cta acc tgt gad aag tgt cca gca gga acc tat gtc tct gag cat tgt 240
Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
15 25 30 35
acc aac aca agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt 288
Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55
acc agg cat gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca 336
Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70
tgc cca tgg cca atg att gag aaa tta cct tgt gct gcc ttg act gac 384
Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
75 80 85
cga gaa tgc act tgc cca cct ggc atg ttc cag tct aac gct acc tgt 432
Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
90 95 100
gcc ccc cat acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg 480
Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105 110 115
aca gag act gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc 528
Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
120 125 130 135
tca gat gtg cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt 576
Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
140 145 150
ctg agt cag aac ctg gtg atc aag ccg ggg acc aag gag aca gac 624
Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
155 160 165
aac gtc tgt ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc 672
Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Thr Ser Pro Ser
170 175 180
cct ggc aca gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa 720
Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
185 190 195
gtc cct tcc tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc 768
Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
200 205 210 215
60

	aac tct tct gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu 220 225 230	816
5	ggg aca gtc cct gac aac aca agc tca gca agg aag gaa gac gtg Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val 235 240 245	864
10	aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro 250 255 260	912
15	cac cac aga cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly 265 270 275	960
	ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro 280 285 290 295	1008
20	aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg ccc ttg Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp 300 305 310	1056
25	atg att gtg ctt ttc ctg ctg gtg ctt gtg gtg att gtg gtg tgc Met Ile Val Leu Phe Leu Leu Val Leu Val Val Ile Val Val Cys 315 320 325	1104
30	agt atc cg ^g aaa agc tcg agg act ctg aaa aag ggg ccc cg ^g cag gat Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp 330 335 340	1152
	ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro 345 350 355	1200
35	acc cag aac cg ^g gag aaa tgg atc tac tac tgc aat ggc cat gga ccc Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro 360 365 370 375	1248
40	cat gat gag gag tgg ggg ttg atg gag aga cat att caa gat att tat His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr 380 385 390	1296
45	att caa aga agc aat caa gat tca gaa aga tgg ggt tgataatttt Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly 395 400	1342
	tacttcaccc tgggaggcag catagtgcag tgaaaggtat cgatatcctg aagctttag 1402	
50	cagcccaagt gggaaagccag tggaaaagata tcatacgat tctttgcaat gccagtgaga 1462	
	gggaggttgc tg	1474
55	<210> 8 <211> 444 <212> PRT <213> primate	
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Sub A²

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Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg
-40 -35 -30

5 Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu
-25 -20 -15 -10

10 Leu Gly Phe Leu Ser Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser
-5 -1 1 5

15 Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val
10 15 20

20 Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys
25 30 35

25 Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe
40 45 50 55

30 Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro
60 65 70

35 Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp
75 80 85

40 Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys
90 95 100

45 Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly
105 110 115

50 Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe
120 125 130 135

55 Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys
140 145 150

60 Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp
155 160 165

65 Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser
170 175 180

70 Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu
185 190 195

75 Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser
200 205 210 215

80 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu
220 225 230

85 Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val
235 240 245

90 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro
250 255 260

95 His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly
265 270 275

Sub A2

280	Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro	290	295
5	Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp	300	310
10	Met Ile Val Leu Phe Leu Leu Val Leu Val Val Ile Val Val Cys	315	325
15	Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp	335	340
20	Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro	345	355
25	Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro	360	375
30	His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr	380	390
35	Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly	395	400
40	<210> 9 <211> 227 <212> PRT <213> rodent		
45	<400> 9 Met Ala Pro Ala Ala Leu Trp Val Ala Leu Val Phe Glu Leu Gln Leu	1	15
50	Trp Ala Thr Gly His Thr Val Pro Ala Gln Val Val Leu Thr Pro Tyr	20	30
55	Lys Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp	35	45
60	Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val	50	60
65	Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu	65	80
70	Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser	70	95
75	Cys Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr	85	100
80	Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala	100	110
85	Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys	115	125
90	130	135	140
95	60 Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn		

Sub A2

145	150	155	160
Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser			
165	170	175	
Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile			
180	185	190	
Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr			
195	200	205	
Leu Ser Ala Ile Pro Arg Thr Leu Tyr Val Ser Gln Pro Glu Pro Thr			
210	215	220	
Arg Ser Gln			
225			
<210> 10			
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<400> 10			
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu			
1	5	10	15
Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr			
20	25	30	
Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln			
35	40	45	
Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys			
50	55	60	
Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp			
65	70	75	80
Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys			
85	90	95	
Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg			
100	105	110	
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu			
115	120	125	
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg			
130	135	140	
Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val			
145	150	155	160
Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr			
165	170	175	
Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly			
180	185	190	

Sub A2

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Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220

Gln
225

<210> 11
<211> 187

<212> PRT
<213> primate

<400> 11

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
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20 Lys, Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
35 40 45

25 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
50 55 60

30 Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
85 90 95

35 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
115 120 125

40 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130 135 140

45 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
165 170 175

50 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly
180 185

<210> 12

<211> 636

<212> DNA

<213> rodent

<220>

60 <221> CDS

<222> (104)..(553)

<220>

<221> mat peptide
<222> (191)..(553)

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10 cagcactggc gagtagcagg aataaacacg tttggtgaga gcc atg gca ctc aag 115
Met Ala Leu Lys15 gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc cta 163
Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe Leu
-25 -20 -15 -1020 ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg cag 211
Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg Gln
-5 -1 1 525 cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag tgc 259
Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln Cys
10 15 2030 gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg gag 307
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu
25 30 3535 gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac tgg 355
Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp Trp
40 45 50 5540 ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac cgc 403
Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn Arg
60 65 7045 ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg gac 451
Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly Asp
75 80 8550 tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa gac 499
Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp
90 95 10055 atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca cac 547
Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Tyr Glu Pro His
105 110 11560 tgt gag tgatgtgcc agtggcagca gactttaaaa aaaaaaagaa aaaaaaacaa 603
Cys Glu
120

acaacaa aaaaaaaaaaaa aaaaaaaaaaaa aaa

636

55

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<211> 150

<212> PRT

<213> rodent

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-25 -20 -15

5 Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
-10 -5 -1 1

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
5 10 15

10 Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
20 25 30 35

15 Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
40 45 50

20 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
55 60 65

25 Leu, Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
70 75 80

30 Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
85 90 95

35 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
100 105 110 115

40 Tyr Glu Pro His Cys Glu
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45 <210> 14
<211> 474
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<213> primate

50 <220>
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<222> (78)..(473)

55 <220>
<221> misc_feature
<222> (308)
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T; translated amino acid depends on genetic code

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ttaccggcct tccccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
1 5 10

65 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga tag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25

70 tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206

Ser Lys Asp Cys Gly Tyr Gly Glu Gly Asp Ala Tyr Cys Thr Ala
30 35 40

tgc cct cct cgc agt aca aaa gca gct ggg gcc acc aca aat gtc aga 254
Cys Pro Pro Arg Ser Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg
45 50 55

gtt gca tca cct gtg ctg tca tca atc gtg ttc aga agg ttc aac tgc 302
Val Ala Ser Pro Val Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys
60 65 70 75

aca gtn acc tct nat gct gtc tgt ggg gga ngg ttt gcc caa gtt tct 350
Thr Xaa Thr Ser Xaa Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser
80 85 90

aac cga aag aca cgc cat tgg aag gct gcc agg acc aag gat ggc atc 398
Asn Arg Lys Thr Arg His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile
95 100 105

ccg tgg cac aaa gnc aga ccc cca act tct gan ggt tnc aaa gtg nct 446
Pro Trp His Lys Xaa Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa
110 115 120

ttc caa ttg gag ctt aat ggg agg can a 474
Phe Gln Leu Glu Leu Asn Gly Arg Xaa
125 130

<210> 15

<211> 132

<212> PRT

<213> primate

<400> 15

Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
1 5 10 15

Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
20 25 30

Tyr Gly Glu Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Ser
35 40 45

Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg Val Ala Ser Pro Val
50 55 60

Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys Thr Xaa Thr Ser Xaa
65 70 75 80

Ala Val Cys Gly Xaa Phe Ala Gln Val Ser Asn Arg Lys Thr Arg
85 90 95

His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile Pro Trp His Lys Xaa
100 105 110

Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa Phe Gln Leu Glu Leu
115 120 125

Asn Gly Arg Xaa
130

Sub A2

5 <210> 16
 <211> 546
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10 <220>
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 <222> (78) ..(308)

15 <220>
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and 541 may be A, C, G, or T

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ttacccggct tccccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
 1 5 10
25 tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
 15 20 25
30 tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Asp Ala Tyr Cys Thr Ala
 30 35 40
35 tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
 45 50 55
40 agt tgc atc acc tgt gct atc aat cgt gtt cag aag gtc caa ctg 302
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu
 60 65 70 75
45 cac agc taacctctna tgctgtctgt gggatgttt gncccaagtt ctnaccgaaa 358
His Ser
50 agacacgcca tggaaaggct ggcaggacca ngtatggccn tcccgtggca gaaagccaga 418
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gcntgcca 546

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Sub A2

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1 5 10 15
Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
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Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
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Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
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Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln
35 1 5 10
tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu
15 20 25
40 tcc aag gat tgt tat gga gag ggt gga gat gcc tac tgc aca gcc 206
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Asp Ala Tyr Cys Thr Ala
30 35 ,40
45 tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln
45 50 55
50 agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc aac tgc 302
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys
60 65 70 75
55 aca gct acc tct aat gct gtc tgt ggg gac tgt ttg ccc agg ttc tac 350
Thr Ala Thr Ser Asn Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr
80 85 90
55 cga aag aca cgc att gga ggc ctg cag gac caa gag tgc atc ccg tgc 398
Arg Lys Thr Arg Ile Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys
95 100 105
60

acg aag cag acc ccc acc tct gag gtt caa tgt gcc ttc cag ttg agc 446
Thr Lys Gln Thr Pro Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser
110 115 120

5 tta gtg gag gca gat gca ccc aca gtg ccc cct cag gag gcc aca ctt 494
Leu Val Glu Ala Asp Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu
125 130 135

10 gtt gca ctg gtg agc agc ctg cta gtg gtg ttt acc ctg gcc ttc ctg 542
Val Ala Leu Val Ser Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu
140 145 150 155

15 ggg ctc ttc ttc ctc tac tgc aag cag ttc ttc aac aga cat tgc cag 590
Gly Leu Phe Phe Leu Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln
160 165 170

20 cgt gga ggt ttg ctg cag ttt gag gct gat aaa aca gca aag gag gaa 638
Arg Gly Gly Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu
175 180 185

25 tct ctc ttc ccc gtg cca ccc agc aag gag acc agt gct gag tcc caa 686
Ser Leu Phe Pro Val Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln
190 195 200

30 gtc tct tgg gcc cct ggc agc ctt gcc cag ttg ttc tct ctg gac tct 734
Val Ser Trp Ala Pro Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser
205 210 215

35 gtt cct ata cca caa cag cag cag ggg cct gaa atg tgatgtccac 780
Val Pro Ile Pro Gln Gln Gln Gly Pro Glu Met
220 225 230

angagcta at accctacaga tggggcatat cctatccat cccaccagag gattgattct 840

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Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
35 40 45

55 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
50 55 60

60 Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
65 70 75 80

Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
85 90 95

Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
100 105 110

Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
115 120 125

Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
130 135 140

Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
145 150 155 160

Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
165 170 175

Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
180 185 190

Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Trp Ala Pro
195 200 205

Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser Val Pro Ile Pro Gln
210 215 220

Gln Gln Gln Gly Pro Glu Met
225 230